

10.5 PLACENTA  
TESTIS  
SEMINAL VESICLE  
OVARY  
OVIDUCT  
UTERUS  
BRAIN  
THYMUS  
HEART  
LUNG  
KIDNEY  
ADRENAL  
SPLEEN  
LIVER  
INTESTINE  
PANCREAS

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PANCREAS

FIG. 1A

8.5  
10.5  
12.5  
14.5  
16.5  
18.5

FIG. 1B

1 TTCAAGCCCTCAGTCAGTTGTGCGGGAGAAAGGGGGGGTTCGGCTTTCTCCTTTCAAGAA  
61 CGAGTTATTTTCAGCTGCTGACTGGAGACGGTGCACGTCTGGACACGGGAGCACCTTCCAC  
121 TATGGGACTGGATACAGACACACGCCGGGACTTCAAGACACTCAGACTGAGGAGAAA  
181 GCCCTGCCCTGCTGCTGCTGCTGCTGCCACCGCTGCCCTCTGAAGACCCACTCCTT  
241 TCATGGTTTTCCTGCCAAGCCAGAGGACCTTCGCTGCTACGGCCTTTCTCTGTGTGT  
301 CATTACGGGCTGGCCAGAGGATGAGACTCCCCAAACTCCTCACTCTTTTGCTGTGGCAC  
M R L P K L L T L L L W H  
361 CTGGCTTGGCTGGACCTGGAACTCATCTGCACCTGTGCTGGGTGCCCTGACTTAGGACAG  
L A W L D L E L I C T V L G A P D L G Q  
421 AGAACCCAGGGGCCAAGCCAGGCTTGACCAAAGCGGAGGCCAAGGAGAGGCCACCCCTG  
R T P G A K P G L T K A E A K E R P P L  
481 GCCAGGAATGCTTTAGGCCAGGGGTCATATCTATGTTGGGGGCCACCAATGCCAGG  
A R N V F R P G G H I Y G V G A T N A R  
541 GCCAAGGGAAGCTCTGGGCAGACACAGGCCCAAGAGGTGAACCCAGAAAGATGCCCCC  
A K G S S G Q T Q A K K D E P R K M P P  
601 AGATCCGGTGGCTCTGAAACCAAGCCAGGACCCCTCTTCCCAGACTAGACAGGCTGCAGCC  
R S G G S E T K P G P S S Q T R Q A A A  
661 CGGACTGTAAACCCCAAGGACAGCTTCTGCGGGCAAGCATCTTCAAAAGCAGGATCT  
R T V T P K G Q L P G G K A S S K A G S  
721 GCCCCAGCTCCTTCTGCTGAAGAAGACAGGAGCCCTGGGACCCCTCGAGAGCCCAAG  
A P S S F L L K K T R E P G T P R E P K  
781 GAGCCGTTCCGCCCCCCCCATCACACCCACGAATACATGCTCTCCCTGTACAGGACG  
E P F R P P P I T P H E Y M L S L Y R T  
841 CTGTCCGATGCTGACAGAAAGGAGGTAAACAGCAGCGTGAAGTTGGAGGCTGGCCCTGGCC  
L S D A D R K G G N S S V K L E A G L A  
901 AACACCATCACCAGCTTTATTGACAAAGGCAAGATGACCGAGGCCCTGCGGTACGGAAG  
N T I T S F I D K G Q D D R G P A V R K  
961 CAGAGGTACGTGTTGACATCAGTCCCTTGGAGAAGGATGGGCTGTGGGGCTGAACCTG  
Q R Y V F D I S A L E K D G L L G A E L  
1021 CGGATCTTACGGAAGAGCCCTTGGACGTGGCCCAAGCCAGCGGTCCCCAGTAGCGGGCGG  
R I L R K K P L D V A K P A V P S S G R  
1081 GTTGCCCAACTGAAGCTGTCCAGCTGCCCCAGCGGGCCGCGGACGCCCTTGTCTGGAT  
V A Q L K L S S C P S G R Q P A A L L D

FIG. 2A



GDF-1 RLRHTEPRVEVGPVGTCTRRRLHVSF-REVGWHRWVIAPRGFLANFCQGTICALPETLRGPGGPP  
 GDF-3 RKRRAAISVPKGFRCNHCRRHQLFINF-QDLGWHKWIAPKGFMANCHGECFESMTTYLNS---  
 GDF-5 PLANRQGRPSKNLKARCSRKALHVNF-KDMGWDDWIAPLEYEAFHCEGLCEFLRSHLEP---  
 GDF-9 SFNLSEYFKQFLFPQNEICELHDFRLSF-SOLKWDNWIAPHRYPNRYCKGDCPRAVRHRYGS---  
 BMP-2 REKRAKHQRKRLKSSCKRHPLYVDF-SDVGWNDWIAPPGYHAFYCHGECPEPLADHLNS---  
 BMP-4 KRSPKHHSQARAKKNKNCRRHSLYVDF-SDVGWNDWIAPPGYQAFYCHGDCPFPLADHLNS---  
 Vgr-1 SRGSGSDYNGSELKACKKHELIVSF-QDLGWQDWIIAPKGYAANYCDGECSCFPLNAHMNA---  
 OP-1 LRMANVAENSSSDQROACKKHELIVSF-RDLGWQDWIIAPEGYAAFYCEGECACFPLNSYMNA---  
 BMP-5 SRMSSVDYNTSEKQACKKHELIVSF-RDLGWQDWIIAPEGYAAFYCDGECSCFPLNAHMNA---  
 BMP-3 EQTLKKARRKQWIEPRNCARRYLVDF-ADIGWSEWIIIPKSFDAFYCSGACQFPMPSLKPS---  
 MIS GPGRAQRSAGATAADGPGCALRELSVDL----RAERSVLIPETYQANCOGVCGWQSDRNPRY---  
 Inhibin ALRLQRPPPEEPAHAHCHRVALNISF-QELGWERWIVPPSFIFHYCHGCGGLHIPNLSLPV-  
 Inhibin HRRRRRGLECDGV-NICCKQFFVSF-KDIGWNDWIAPSGYHANYCEGECPSHIAGTSGSSL-  
 Inhibin HRIKRGLECDGRT-NLCRQQFFIDF-RDIGWNDWIAPTYGYGNYCEGSCPAYLAGVPGSAS-  
 TGF- $\beta$ 1 HRRALDTNYCESSTEKNCCVRQYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD-----  
 TGF- $\beta$ 2 KKRALDAAYCFRNVDNCCLRPLYIDFRKDLGWK-WIHEPKGYANFACAGACPYLWSSD-----  
 TGF- $\beta$ 3 KKRALDTNYCFRNLEENCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPPPYLRSAD-----

GDF-1 ALNHAVLRALMHA-AAPTGGAGSPCCV--PERLSPISVLFF-DNSDNVVLRYHEDMVVDECGCR  
 GDF-3 -SNYAFMQALMHM---ADPKVPKAVCV--PTKLSPI SMLYQ-DSKDNVILRYHEDMVVDECGCG  
 GDF-5 -TNHAVIQTLMNS--MDPESTPTCCV--PTRLSPISILFI-DSANNVYKQYEDMVVESCGCR  
 GDF-9 -PVHTMVQNIIE--KLDPSVPRPSCV--PGKYSPLSVLTI-EPDGSIAKEYEDMIATRCTCR  
 BMP-2 -TNHAI VQTLVNS---VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR  
 BMP-4 -TNHAI VQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR  
 Vgr-1 -TNHAI VQTLVHL--MNPEYVPKPCA--PTKLNATSVLYF-DDNSNVILKKYRNMMVVRACGCH  
 OP-1 -TNHAI VQTLVHF--INPETVPKPCA--PTQLNATSVLYF-DDSSNVILKKYRNMMVVRACGCH  
 BMP-5 -TNHAI VQTLVHL--MFPDHPKPCA--PTKLNATSVLYF-DDSSNVILKKYRNMMVVRSCGCH  
 BMP-3 --NHATIQSIVRA-VGVVPGIPEPCV--PEKMSSLSILFF-DENKNVILKYPNMTVESACACR  
 MIS -GNHVLLLLKMQA--RGAALARPPCCV--PTAYAGKLLISLSEER--ISAHVPNMVAIECGCR  
 Inhibin -PGAPPTPAQPSY----LLPGAQPCCAALPGTMRPLHVRTISDGGYSFKYETVPNLLTOHCACI  
 Inhibin -SFHSTVINHYRMGRGSHFANLKSCCV--PTKL RPSMMLY- DDGQNIKKDIQNMIVEECGCS  
 Inhibin -SFHTAVNQYRMGRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA  
 TGF- $\beta$ 1 -TQYSKVLALYNQ--HNPGASAAPCCV--PQALEPLPIVYV-VGRKPKV-EQLSNMIVRSCKCS  
 TGF- $\beta$ 2 -TQHSRVLSLYNT--INPEASASPCCV--SODLEPLTILYY-IGKTPKI-EQLSNMIVKSKCS  
 TGF- $\beta$ 3 -TTHSTVLGLYNT--LNPEASASPCCV--PODLEPLTILYY-VGRTPKV-EQLSNMIVKSKCS

FIG. 3A

SEQ ID NO: 28  
 SEQ ID NO: 29  
 SEQ ID NO: 30

SEQ ID NO: 28	GDF-5	371	R	R	K	R	R	A	P	L	A	N	R	Q	G	K	R	P	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	395	K	N	L	K	A	R	C	S		
SEQ ID NO: 29	GDF-6		R	R	R	R	R	T	A	F	A	S	R	H	G	K	R	H	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		K	S	R	L	R	C	S				
SEQ ID NO: 30	GDF-7		R	R	R	R	R	T	A	L	A	G	T	R	G	A	Q	G	S	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	R	G	H	G	R	S	R	C	S

GDF-5	396	R	K	A	L	H	V	N	F	K	D	M	G	W	D	D	W	I	I	A	P	L	E	Y	E	A	F	H	C	E	G	L	C	E	F	P	L	R	S	H	L	E	P	T	N	H	A	V	I	Q	T	L
GDF-6		R	K	P	L	H	V	N	F	K	E	L	G	W	D	D	W	I	I	A	P	L	E	Y	E	A	Y	H	C	E	G	V	C	D	F	P	L	R	S	H	L	E	P	T	N	H	A	I	I	Q	T	L
GDF-7		R	K	S	L	H	V	D	F	K	E	L	G	W	D	D	W	I	I	A	P	L	D	Y	E	A	Y	H	C	E	G	V	C	D	F	P	L	R	S	H	L	E	P	T	N	H	A	I	I	Q	T	L

GDF-5	447	M	N	S	M	D	P	E	S	T	P	P	T	C	C	V	P	T	R	L	S	P	I	S	I	L	F	I	D	S	A	N	N	V	V	Y	K	Q	Y	E	D	M	V	V	E	S	C	G	C	R
GDF-6		M	N	S	M	D	P	G	S	T	P	P	S	C	C	V	P	T	K	L	T	P	I	S	I	L	Y	I	D	A	G	N	N	V	V	Y	K	Q	Y	E	D	M	V	V	E	S	C	G	C	R
GDF-7		L	N	S	M	A	P	D	A	A	P	A	S	C	C	V	P	A	R	L	S	P	I	S	I	L	Y	I	D	A	A	N	N	V	V	Y	K	Q	Y	E	D	M	V	V	E	A	C	G	C	R

FIG.3B

FIG. 4

GDF-1	100	33	50	46	44	48	35	27	42	43	46	47	46	42	34	23	37	36	33	TGF- $\beta$ 3
GDF-2	-	100	42	47	51	48	31	32	52	51	55	52	55	34	20	20	32	25	26	TGF- $\beta$ 2
GDF-3	-	-	100	49	49	46	41	33	53	50	53	50	50	42	22	26	42	41	36	TGF- $\beta$ 1
GDF-5	-	-	-	-	-	-	37	33	57	57	51	51	52	47	27	26	40	37	33	Inhibin $\beta$ B
GDF-6	-	-	-	-	-	-	38	34	57	56	53	53	54	46	26	27	43	39	35	Inhibin $\beta$ A
GDF-7	-	-	-	-	-	-	37	33	57	57	52	53	52	46	25	26	41	36	36	Inhibin $\alpha$
GDF-8	-	-	-	-	-	-	100	27	41	38	45	42	42	38	31	26	38	42	34	MIS
GDF-9	-	-	-	-	-	-	-	100	33	34	31	30	31	29	21	27	30	31	23	BMP-3
BMP-2	-	-	-	-	-	-	-	-	100	92	61	60	61	48	27	22	42	42	35	BMP-5
BMP-4	-	-	-	-	-	-	-	-	-	100	60	58	59	47	27	22	41	42	34	OP-1
Vgr-1	-	-	-	-	-	-	-	-	-	-	100	87	91	44	24	25	44	41	35	Vgr-1
OP-1	-	-	-	-	-	-	-	-	-	-	-	100	88	42	27	24	43	42	34	OP-1
BMP-5	-	-	-	-	-	-	-	-	-	-	-	-	100	43	24	24	43	37	34	BMP-5
BMP-3	-	-	-	-	-	-	-	-	-	-	-	-	-	100	30	29	36	37	32	BMP-3
MIS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	18	24	25	28	MIS
Inhibin $\alpha$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	26	25	23	Inhibin $\alpha$
Inhibin $\beta$ A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	63	41	Inhibin $\beta$ A
Inhibin $\beta$ B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	35	Inhibin $\beta$ B
TGF- $\beta$ 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	TGF- $\beta$ 1
TGF- $\beta$ 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	TGF- $\beta$ 2
TGF- $\beta$ 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	TGF- $\beta$ 3

FIG. 5A



FIG. 5B

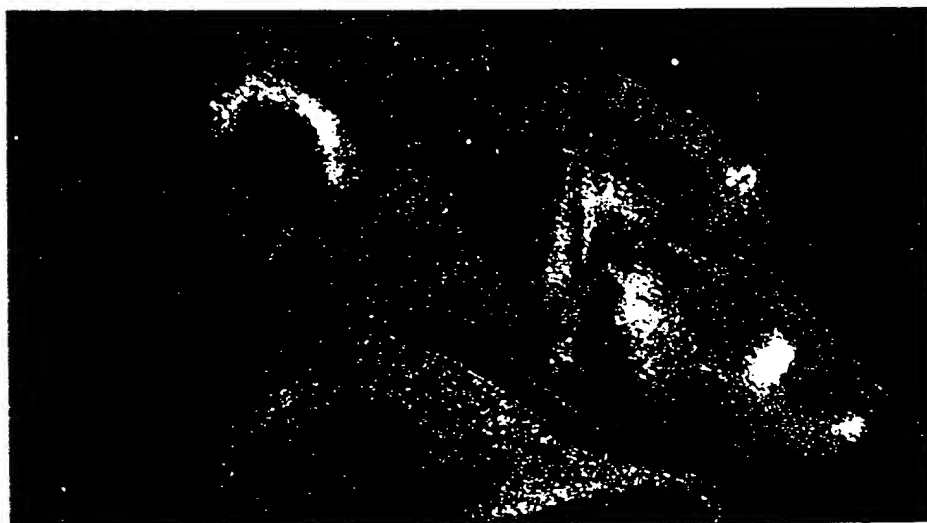


FIG. 5C



FIG. 5D

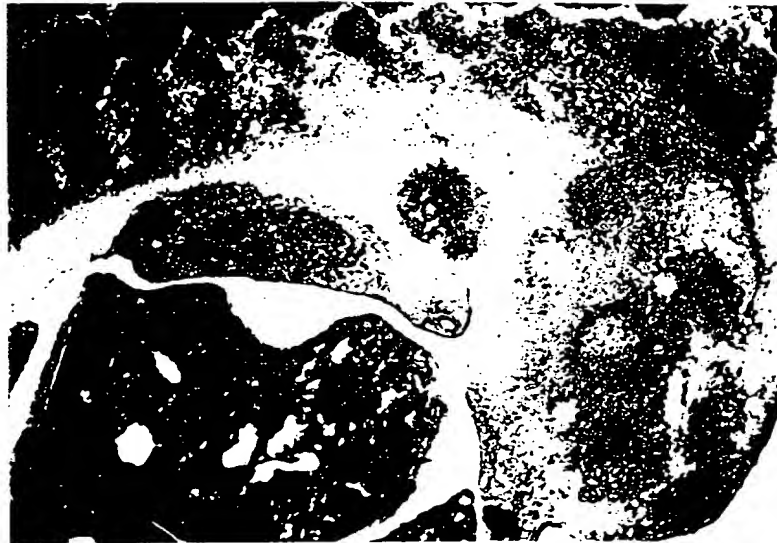


FIG. 5E

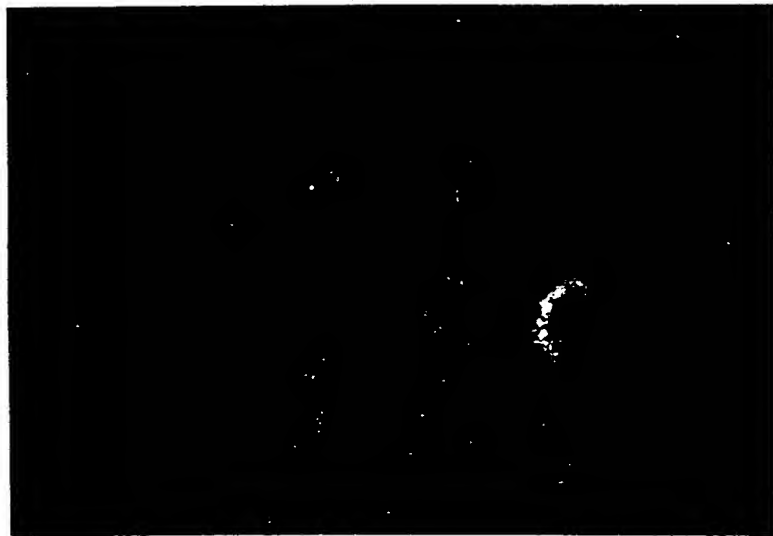


FIG. 5F





FIG. 6A

FIG. 6B

A high-contrast, black and white photograph showing a close-up of a person's face. The image is heavily shadowed and distorted, possibly due to a mask or severe facial injury. The lighting is harsh, creating deep blacks and bright whites, with very little mid-tone detail. The features are difficult to discern but appear to be in a state of extreme tension or distress. The overall effect is graphic and unsettling.